5/20 #4

OIPE

RAW SEQUENCE LISTING   DATE: 04/07/2003
PATENT APPLICATION: **US/09/882,227**   TIME: 09:47:31

Input Set : **N:\vernette\US09882227.raw**
Output Set: **N:\CRF4\04072003\I882227.raw**

```
 1 <110> APPLICANT: Kleanthous, Harold
 2        Al-Garawi, Amal
 3        Miller, Charles
 4        Tomb, Jean-Francois
 5        Ooomen, Raymond P.
 6 <120> TITLE OF INVENTION: Identification of Polynucleotides
 7        Encoding Novel Helicobacter Polypeptides in the Helicobacter
 8        Genome
 9 <130> FILE REFERENCE: 06132/047002
10 <140> CURRENT APPLICATION NUMBER: US/09/882,227
11 <141> CURRENT FILING DATE: 2001-06-15
12 <150> PRIOR APPLICATION NUMBER: US 08/902,615
13 <151> PRIOR FILING DATE: 1997-07-29
14 <160> NUMBER OF SEQ ID NOS: 638
15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1613
19 <212> TYPE: DNA
20 <213> ORGANISM: Helicobacter pylori
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (64)...(1551)
24 <400> SEQUENCE: 1
25     taagaaaaac cgctagagtg caatacaatt cttgaaagat atgaaattaa aaaaggagac 60
26     ttt atg tta aaa atc aaa tta gaa aaa acc act ttt gaa aac gca aaa   108
27         Met Leu Lys Ile Lys Leu Glu Lys Thr Thr Phe Glu Asn Ala Lys
28          1               5                  10                  15
29     gct gaa tgc agt tta gtt ttt att atc aat aag gat ttt agc cac gct   156
30     Ala Glu Cys Ser Leu Val Phe Ile Ile Asn Lys Asp Phe Ser His Ala
31                      20                  25                  30
32     tgg gtc aaa aat aaa gag ttg cta gaa acc ttt aaa tac gaa ggc gaa   204
33     Trp Val Lys Asn Lys Glu Leu Leu Glu Thr Phe Lys Tyr Glu Gly Glu
34                      35                  40                  45
35     ggc gta ttt tta gac caa gaa aat aaa atc ctg tat gcg ggc gtt aaa   252
36     Gly Val Phe Leu Asp Gln Glu Asn Lys Ile Leu Tyr Ala Gly Val Lys
37                  50                  55                  60
38     gaa gat gat gtg cat tta ttg aga gag agc gcg tgt tta gcc gtt cgc   300
39     Glu Asp Asp Val His Leu Leu Arg Glu Ser Ala Cys Leu Ala Val Arg
40              65                  70                  75
41     acc ctt aaa aaa ctc gct ttt aaa agc gtt aaa gtg ggc gtt tat act   348
42     Thr Leu Lys Lys Leu Ala Phe Lys Ser Val Lys Val Gly Val Tyr Thr
43      80                  85                  90                  95
44     tgt ggt gca cat tct aaa gat aac gcg ctt tta gaa aac ttg aaa gcg   396
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45    Cys Gly Ala His Ser Lys Asp Asn Ala Leu Leu Glu Asn Leu Lys Ala
46                    100             105             110
47    ctg ttt ttg ggc ttg aaa tta ggt ttg tat gaa tac gac act ttt aaa    444
48    Leu Phe Leu Gly Leu Lys Leu Gly Leu Tyr Glu Tyr Asp Thr Phe Lys
49                    115             120             125
50    tcc aac aaa aaa gaa agc gtt tta aaa gaa gcc att gtc gct tta gaa    492
51    Ser Asn Lys Lys Glu Ser Val Leu Lys Glu Ala Ile Val Ala Leu Glu
52                130             135             140
53    ttg cac aaa cct tgc gaa aaa act tgc gca aat tct tta gaa aag agt    540
54    Leu His Lys Pro Cys Glu Lys Thr Cys Ala Asn Ser Leu Glu Lys Ser
55            145             150             155
56    gct aaa gaa gcg tta aaa tac gct gaa atc atg aca gaa agc ttg aat    588
57    Ala Lys Glu Ala Leu Lys Tyr Ala Glu Ile Met Thr Glu Ser Leu Asn
58    160             165             170             175
59    atc gtt aaa gat cta gtc aat acc ccc cct atg att ggc act ccg gtt    636
60    Ile Val Lys Asp Leu Val Asn Thr Pro Pro Met Ile Gly Thr Pro Val
61                    180             185             190
62    tat atg gct gaa gtg gcg caa aaa gtg gct aaa gaa aac cat tta gaa    684
63    Tyr Met Ala Glu Val Ala Gln Lys Val Ala Lys Glu Asn His Leu Glu
64                    195             200             205
65    atc cat gtt cat gat gaa aaa ttt tta gaa gaa aag aaa atg aac gcc    732
66    Ile His Val His Asp Glu Lys Phe Leu Glu Glu Lys Lys Met Asn Ala
67                    210             215             220
68    ttt tta gcg gtc aat aaa gcc tct ctt agc gtc aat cct cct cgc ttg    780
69    Phe Leu Ala Val Asn Lys Ala Ser Leu Ser Val Asn Pro Pro Arg Leu
70            225             230             235
71    atc cat tta gtc tat aag cct aaa aaa gcg aag aaa aaa atc gct tta    828
72    Ile His Leu Val Tyr Lys Pro Lys Lys Ala Lys Lys Lys Ile Ala Leu
73    240             245             250             255
74    gtg ggt aag ggc ttg act tat gat tgt ggg ggt ttg agc ttg aaa ccg    876
75    Val Gly Lys Gly Leu Thr Tyr Asp Cys Gly Gly Leu Ser Leu Lys Pro
76                    260             265             270
77    gcc gat tac atg gtt act atg aaa gcg gat aaa ggc ggt ggc tct gcg    924
78    Ala Asp Tyr Met Val Thr Met Lys Ala Asp Lys Gly Gly Gly Ser Ala
79                    275             280             285
80    gtg att ggg ctt tta aac gca tta gcc aaa cta ggc gtg gag gct gaa    972
81    Val Ile Gly Leu Leu Asn Ala Leu Ala Lys Leu Gly Val Glu Ala Glu
82                290             295             300
83    gtg cat ggc att att ggg gct aca gaa aac atg ata ggc cca gcc gct    1020
84    Val His Gly Ile Ile Gly Ala Thr Glu Asn Met Ile Gly Pro Ala Ala
85            305             310             315
86    tat aaa cca gat gat att ttg atc tcc aaa gaa ggc aag agc ata gag    1068
87    Tyr Lys Pro Asp Asp Ile Leu Ile Ser Lys Glu Gly Lys Ser Ile Glu
88    320             325             330             335
89    gtc cgt aat acc gac gct gag ggg cgt ttg gtt tta gcg gat tgt ttg    1116
90    Val Arg Asn Thr Asp Ala Glu Gly Arg Leu Val Leu Ala Asp Cys Leu
91                340             345             350
92    agc tac gct caa gat tta aac cct gat gtg atc gtg gat ttt gcg acc    1164
93    Ser Tyr Ala Gln Asp Leu Asn Pro Asp Val Ile Val Asp Phe Ala Thr
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Input Set : N:\vernette\US09882227.raw
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 94                 355              360              365
 95     ctt act ggg gca tgc gtt gta ggc tta ggc gaa ttc act tca gcg atc   1212
 96     Leu Thr Gly Ala Cys Val Val Gly Leu Gly Glu Phe Thr Ser Ala Ile
 97             370              375              380
 98     atg ggg cat aat gaa gag tta aaa aac ctc ttt gaa act tca ggg tta   1260
 99     Met Gly His Asn Glu Glu Leu Lys Asn Leu Phe Glu Thr Ser Gly Leu
100         385              390              395
101      gaa tcc ggc gaa tta tta gcc aaa ctc ccc ttt aac cgc cat tta aag   1308
102      Glu Ser Gly Glu Leu Leu Ala Lys Leu Pro Phe Asn Arg His Leu Lys
103      400              405              410              415
104      aaa ttg att gaa tct aaa atc gct gat gtg tgc aat att tct tct tca   1356
105      Lys Leu Ile Glu Ser Lys Ile Ala Asp Val Cys Asn Ile Ser Ser Ser
106                   420              425              430
107      cgc tat ggc ggt gcg atc aca gcg ggc ttg ttt tta aat gaa ttt att   1404
108      Arg Tyr Gly Gly Ala Ile Thr Ala Gly Leu Phe Leu Asn Glu Phe Ile
109                   435              440              445
110      aga gat gag ttt aag gat aag tgg cta cac att gac att gca ggc cct   1452
111      Arg Asp Glu Phe Lys Asp Lys Trp Leu His Ile Asp Ile Ala Gly Pro
112              450              455              460
113      gct tat gtg gaa aaa gaa tgg gat gtg aat agc ttt gga gcg agt ggg   1500
114      Ala Tyr Val Glu Lys Glu Trp Asp Val Asn Ser Phe Gly Ala Ser Gly
115          465              470              475
116      gct ggc gtg aga gct tgc aca gct ttt gtg gaa gag ctt ttg aaa aag   1548
117      Ala Gly Val Arg Ala Cys Thr Ala Phe Val Glu Glu Leu Leu Lys Lys
118      480              485              490              495
119      gct tgaaatgggc ttgtctgtag gcattgtggg tttgcctaat gtgggcaaat        1601
120      Ala
121      ccagcacctt ta                                                     1613
123 <210> SEQ ID NO: 2
124 <211> LENGTH: 496
125 <212> TYPE: PRT
126 <213> ORGANISM: Helicobacter pylori
127 <400> SEQUENCE: 2
128      Met Leu Lys Ile Lys Leu Glu Lys Thr Thr Phe Glu Asn Ala Lys Ala
129      1               5                   10                  15
130      Glu Cys Ser Leu Val Phe Ile Ile Asn Lys Asp Phe Ser His Ala Trp
131                  20                  25                  30
132      Val Lys Asn Lys Glu Leu Leu Glu Thr Phe Lys Tyr Glu Gly Glu Gly
133                  35                  40                  45
134      Val Phe Leu Asp Gln Glu Asn Lys Ile Leu Tyr Ala Gly Val Lys Glu
135          50                  55                  60
136      Asp Asp Val His Leu Leu Arg Glu Ser Ala Cys Leu Ala Val Arg Thr
137      65                  70                  75                  80
138      Leu Lys Lys Leu Ala Phe Lys Ser Val Lys Val Gly Val Tyr Thr Cys
139                  85                  90                  95
140      Gly Ala His Ser Lys Asp Asn Ala Leu Leu Glu Asn Leu Lys Ala Leu
141                  100                 105                 110
142      Phe Leu Gly Leu Lys Leu Gly Leu Tyr Glu Tyr Asp Thr Phe Lys Ser
143                  115                 120                 125
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144          Asn Lys Lys Glu Ser Val Leu Lys Glu Ala Ile Val Ala Leu Glu Leu
145              130             135             140
146          His Lys Pro Cys Glu Lys Thr Cys Ala Asn Ser Leu Glu Lys Ser Ala
147          145             150             155             160
148          Lys Glu Ala Leu Lys Tyr Ala Glu Ile Met Thr Glu Ser Leu Asn Ile
149              165             170             175
150          Val Lys Asp Leu Val Asn Thr Pro Pro Met Ile Gly Thr Pro Val Tyr
151              180             185             190
152          Met Ala Glu Val Ala Gln Lys Val Ala Lys Glu Asn His Leu Glu Ile
153              195             200             205
154          His Val His Asp Glu Lys Phe Leu Glu Glu Lys Lys Met Asn Ala Phe
155          210             215             220
156          Leu Ala Val Asn Lys Ala Ser Leu Ser Val Asn Pro Pro Arg Leu Ile
157          225             230             235             240
158          His Leu Val Tyr Lys Pro Lys Lys Ala Lys Lys Lys Ile Ala Leu Val
159              245             250             255
160          Gly Lys Gly Leu Thr Tyr Asp Cys Gly Gly Leu Ser Leu Lys Pro Ala
161              260             265             270
162          Asp Tyr Met Val Thr Met Lys Ala Asp Lys Gly Gly Gly Ser Ala Val
163              275             280             285
164          Ile Gly Leu Leu Asn Ala Leu Ala Lys Leu Gly Val Glu Ala Glu Val
165              290             295             300
166          His Gly Ile Ile Gly Ala Thr Glu Asn Met Ile Gly Pro Ala Ala Tyr
167          305             310             315             320
168          Lys Pro Asp Asp Ile Leu Ile Ser Lys Glu Gly Lys Ser Ile Glu Val
169              325             330             335
170          Arg Asn Thr Asp Ala Glu Gly Arg Leu Val Leu Ala Asp Cys Leu Ser
171              340             345             350
172          Tyr Ala Gln Asp Leu Asn Pro Asp Val Ile Val Asp Phe Ala Thr Leu
173              355             360             365
174          Thr Gly Ala Cys Val Val Gly Leu Gly Glu Phe Thr Ser Ala Ile Met
175              370             375             380
176          Gly His Asn Glu Glu Leu Lys Asn Leu Phe Glu Thr Ser Gly Leu Glu
177          385             390             395             400
178          Ser Gly Glu Leu Leu Ala Lys Leu Pro Phe Asn Arg His Leu Lys Lys
179              405             410             415
180          Leu Ile Glu Ser Lys Ile Ala Asp Val Cys Asn Ile Ser Ser Ser Arg
181              420             425             430
182          Tyr Gly Gly Ala Ile Thr Ala Gly Leu Phe Leu Asn Glu Phe Ile Arg
183              435             440             445
184          Asp Glu Phe Lys Asp Lys Trp Leu His Ile Asp Ile Ala Gly Pro Ala
185              450             455             460
186          Tyr Val Glu Lys Glu Trp Asp Val Asn Ser Phe Gly Ala Ser Gly Ala
187          465             470             475             480
188          Gly Val Arg Ala Cys Thr Ala Phe Val Glu Glu Leu Leu Lys Lys Ala
189              485             490             495
191 <210> SEQ ID NO: 3
192 <211> LENGTH: 560
193 <212> TYPE: DNA
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194 <213> ORGANISM: Helicobacter pylori
195 <220> FEATURE:
196 <221> NAME/KEY: CDS
197 <222> LOCATION: (49)...(492)
198 <400> SEQUENCE: 3
199     ggcgaaatcg ggttaatttt agcagggatt gccagctata ccggtcat atg cat tta   57
200                                                              Met His Leu
201                                                               1
202     ggg tta gcc att tta gtc gca ggg att ggg ggc ttt gtg ggg gat cag   105
203     Gly Leu Ala Ile Leu Val Ala Gly Ile Gly Gly Phe Val Gly Asp Gln
204          5                  10                  15
205     atc tat ttt tac atc ggc cgc acc aat aaa gct tac atc caa aaa aag   153
206     Ile Tyr Phe Tyr Ile Gly Arg Thr Asn Lys Ala Tyr Ile Gln Lys Lys
207      20                  25                  30                  35
208     cta gaa aaa caa cgc cga aaa cta gcc cta gcc cat tta ttg ttg caa   201
209     Leu Glu Lys Gln Arg Arg Lys Leu Ala Leu Ala His Leu Leu Leu Gln
210                  40                  45                  50
211     aaa cac ggc tgg ttt atc att ttt atc caa cgc tat atg tat ggc atg   249
212     Lys His Gly Trp Phe Ile Ile Phe Ile Gln Arg Tyr Met Tyr Gly Met
213                  55                  60                  65
214     cgc acc atc att ccc att agc ata ggt ctc acg cgt tat agc gct tta   297
215     Arg Thr Ile Ile Pro Ile Ser Ile Gly Leu Thr Arg Tyr Ser Ala Leu
216              70                  75                  80
217     aaa ttc gct atc atc aat ctc att agc gcg atg gtg tgg gcg agc att   345
218     Lys Phe Ala Ile Ile Asn Leu Ile Ser Ala Met Val Trp Ala Ser Ile
219              85                  90                  95
220     acc att att cta gcg tgg tat tta gga gaa gag tta ttg cat gcg tta   393
221     Thr Ile Ile Leu Ala Trp Tyr Leu Gly Glu Glu Leu Leu His Ala Leu
222     100                 105                 110                 115
223     ggg tgg ctt aaa aaa cac cct tat gcg cta ata tta cta tta gta tct   441
224     Gly Trp Leu Lys Lys His Pro Tyr Ala Leu Ile Leu Leu Leu Val Ser
225                 120                 125                 130
226     ttc ttg gcg tta gtg ctg tgg tat ttc caa tac tat agt aag aaa aac   489
227     Phe Leu Ala Leu Val Leu Trp Tyr Phe Gln Tyr Tyr Ser Lys Lys Asn
228                 135                 140                 145
229     cgc tagagtgcaa tacaattctt gaaagatatg aaattaaaaa aggagacttt        542
230     Arg
231     atgttaaaaa tcaaatta                                               560
233 <210> SEQ ID NO: 4
234 <211> LENGTH: 148
235 <212> TYPE: PRT
236 <213> ORGANISM: Helicobacter pylori
237 <400> SEQUENCE: 4
238     Met His Leu Gly Leu Ala Ile Leu Val Ala Gly Ile Gly Gly Phe Val
239      1                  5                  10                  15
240     Gly Asp Gln Ile Tyr Phe Tyr Ile Gly Arg Thr Asn Lys Ala Tyr Ile
241                  20                  25                  30
242     Gln Lys Lys Leu Glu Lys Gln Arg Arg Lys Leu Ala Leu Ala His Leu
243                  35                  40                  45
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/07/2003
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:25; N Pos. 42,47
Seq#:27; N Pos. 920
Seq#:27; Xaa Pos. 301
Seq#:28; Xaa Pos. 301
Seq#:77; Xaa Pos. 304
Seq#:78; Xaa Pos. 304
Seq#:81; Xaa Pos. 32
Seq#:82; Xaa Pos. 32
Seq#:85; N Pos. 495
Seq#:86; Xaa Pos. 153
Seq#:103; N Pos. 71
Seq#:103; Xaa Pos. 17
Seq#:104; Xaa Pos. 17
Seq#:127; Xaa Pos. 6
Seq#:128; Xaa Pos. 6
Seq#:137; Xaa Pos. 12
Seq#:138; Xaa Pos. 12
Seq#:139; N Pos. ·479,480,481,482,483
Seq#:139; Xaa Pos. 146,147,148
Seq#:140; Xaa Pos. 146,147,148
Seq#:143; N Pos. 9,12
Seq#:144; Xaa Pos. 3,4
Seq#:145; N Pos. 976,979
Seq#:145; Xaa Pos. 315,316
Seq#:146; Xaa Pos. 315,316
Seq#:153; N Pos. 409,457
Seq#:153; Xaa Pos. 128,144
Seq#:154; Xaa Pos. 128,144
Seq#:165; N Pos. 1028
Seq#:166; Xaa Pos. 326
Seq#:171; N Pos. 48
Seq#:171; Xaa Pos. 8
Seq#:172; Xaa Pos. 8
Seq#:277; Xaa Pos. 81
Seq#:278; Xaa Pos. 81
Seq#:305; N Pos. 388
Seq#:305; Xaa Pos. 118
Seq#:306; Xaa Pos. 118
Seq#:401; Xaa Pos. 217
Seq#:402; Xaa Pos. 217
Seq#:425; Xaa Pos. 182
Seq#:426; Xaa Pos. 182
Seq#:461; N Pos. 375
Seq#:461; Xaa Pos. 123

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Input Set : **N:\vernette\US09882227.raw**
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Seq#:462; Xaa Pos. 123
Seq#:553; N Pos. 528
Seq#:553; Xaa Pos. 172
Seq#:554; Xaa Pos. 172
Seq#:585; Xaa Pos. 66
Seq#:586; Xaa Pos. 66,102
Seq#:589; Xaa Pos. 171

VERIFICATION SUMMARY
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Input Set : **N:\vernette\US09882227.raw**
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L:1033 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:1164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:915
M:341 Repeated in SeqNo=27
L:1214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:288
L:4099 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:77
L:4099 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77 after pos.:963
L:4233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78 after pos.:288
L:4414 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:81
L:4414 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81 after pos.:150
L:4453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82 after pos.:16
L:4649 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:486
L:4687 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86 after pos.:144
L:5530 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103 after pos.:51
M:341 Repeated in SeqNo=103
L:5622 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:104 after pos.:16
L:6938 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:127
L:6938 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:127 after pos.:51
L:6998 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:128 after pos.:0
L:7439 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:137
L:7439 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:137 after pos.:158
L:7503 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:138 after pos.:0
L:7581 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:139 after pos.:440
M:341 Repeated in SeqNo=139
L:7661 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:140 after pos.:144
L:7803 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:143 after pos.:0
L:7859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:144 after pos.:0
L:7962 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:145 after pos.:966
M:341 Repeated in SeqNo=145
L:8014 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:146 after pos.:304
L:8269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:153 after pos.:390
M:341 Repeated in SeqNo=153
L:8300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:154 after pos.:112
M:341 Repeated in SeqNo=154
L:8829 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:165 after pos.:1016
L:8889 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:166 after pos.:320
L:9044 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:171 after pos.:0
M:341 Repeated in SeqNo=171
L:9106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:172 after pos.:0
L:15077 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:277
L:15077 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:277 after pos.:294
L:15149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:278 after pos.:80
L:16693 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:305 after pos.:342
M:341 Repeated in SeqNo=305
L:16750 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:306 after pos.:112
L:22420 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:401
L:22420 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:401 after pos.:675
L:22480 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:402 after pos.:208
L:23803 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:425
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VERIFICATION SUMMARY
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L:23803 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:425 after pos.:582
L:23841 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:426 after pos.:176
L:25953 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:461 after pos.:337
M:341 Repeated in SeqNo=461
L:26065 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:462 after pos.:112
L:31225 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:537,Line#:0
L:32226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:553 after pos.:482
M:341 Repeated in SeqNo=553
L:32272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:554 after pos.:160
L:34202 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:585
L:34202 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:585 after pos.:243
L:34339 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:589
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